UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/090,698	03/04/2002	Joseph Murray	AGYT-011CIP2	5398

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EXAMINER
KIM, YOUNG J

ART UNIT	PAPER NUMBER
1637	

DATE MAILED: 01/02/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 10/03)

Office Action Summary	Application N .	Applicant(s)
	10/090,698	MURRAY ET AL.
	Examiner	Art Unit	
	Young J. Kim	1637	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE _3_ MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**.   2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) _1-20_ is/are pending in the application.

    4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) _1-20_ is/are rejected.

7)☒ Claim(s) _16-20_ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on _04 March 2002_ is/are: a)☒ accepted or b)☐ objected to by the Examiner.

    Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

    Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. §§ 119 and 120

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

    a)☐ All b)☐ Some * c)☐ None of:

      1.☐ Certified copies of the priority documents have been received.

      2.☐ Certified copies of the priority documents have been received in Application No. _____.

      3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

    * See the attached detailed Office action for a list of the certified copies not received.

13)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application) since a specific reference was included in the first sentence of the specification or in an Application Data Sheet. 37 CFR 1.78.

    a) ☐ The translation of the foreign language provisional application has been received.

14)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121 since a specific reference was included in the first sentence of the specification or in an Application Data Sheet. 37 CFR 1.78.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)

2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _4/26/02_ .

4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .

5) ☐ Notice of Informal Patent Application (PTO-152)

6) ☐ Other: .

DETAILED ACTION

Priority

The specification is objected to because the first line of the specification appears to contain a typographical error in the parent PCT application number. Specifically, on page 1, section [01] of the specification, the phrase, "PCT Patent Application No. PCT/US/20603" appears to be in error. According to the PALM record, it appears that the PCT application number is "PCT/US*00*/20603."

Additionally, the priority claim language is appears to be incorrect. On page 1 of the specification, the phrase, "[t]his application claims priority to and is a continuation-in-part application of non-provisional Patent Application No. 09/365,587, entitled "SYSTEM AND METHOD FOR IDENTIFYING CRITICAL REGULATED GENES" filed July 30, 1999, *which is a continuation-in-part application of PCT Patent Application No. PCT/US/20603, [sic] entitled "TECHNIQUES FOR FACILITATING IDENTIFICATION OF CANDIDATE GENES" filed July 28, 2000*," because application number 09/365,587 cannot be a CIP of a later filed said PCT application. The phrase should read, "*and is a continuation-in-part application*," since the instant application is a CIP of said PCT application.

Lastly, Applicants are advised to update the status of the parent application, serial number 09/365,587, as it has become abandoned.

Appropriate correction is required.

Finally, Applicants are advised that the parent application, 09/365,587 does not have support under 112, 1st paragraph for the instant limitation of "using information extraction

algorithm" which retrieve and extract pathway information from databases, rendering the

effective filing date of the instant application, the actual filing date of March 5, 2002.

Applicants are advised that page 23 of the specification contains a reference to a URL.

While information on web-address is accessible, the embedded hyperlinks and/or other forms of

browser-executable code are impermissible and require deletion. The attempt to incorporate

subject matter into the patent application by reference to a hyperlink and/or other forms of

browser-executable code is considered to be an improper incorporation by reference. See MPEP

608.01(p), paragraph I regarding incorporation by reference.

If the subject matter which is improperly incorporated by reference is directed to

nonessential material (illustrating the state of the art), the deletion will probably not be

considered as new matter. However, if the subject matter which is improperly incorporated by

reference is directed to essential material, applicant will be required to amend the specification to

include the subject matter incorporated. The amendment must be accompanied by an affidavit or

declaration executed by the applicant stating that the amendatory material consists of the same

material incorporated by reference.

Information Disclosure Statement

The IDS received on August 26, 2002 is acknowledged and the signed copy of its

corresponding PTO-1449 is attached hereto.

Drawings

Drawings filed on March 4, 2002 are acceptable.

Claim Objections

Claims 16-20 are objected to because of the following informalities:

Independent claims 16 and 20 are missing a punctuation and conjunction, "; and" after

the recitation of the first element of the data processing system, "a processor."

Appropriate correction is required.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the
subject matter which the applicant regards as his invention.

Claims 1-15 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for

failing to particularly point out and distinctly claim the subject matter which applicant regards as

the invention.

Claim 1 (and the dependent claims 2-15) are rejected under 35 U.S.C. 112, second

paragraph, as being incomplete for omitting essential steps, such omission amounting to a gap

between the steps. See MPEP § 2172.01. The omitted steps are the following: After the group

of sequences are identified for further analysis, the next step recites that information extraction

algorithms are used to retrieve and extract pathway information from a database comprising

biological data. However, the group of sequences is not correlated to the information extraction

algorithm. Therefore, it is unclear how the group of sequences is used in the method once they

have been identified, amounting to a gap between the steps. For the purpose of prosecution, the

extracted pathway information of the above-recited step is regarding the group of sequences

which were previously identified for further analysis.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the

basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 16-20 are rejected under 35 U.S.C. 102(b) as being anticipated by Koza et al.

(U.S. Patent No. 5,390,282, issued February 14, 1995).

The instant rejection is predicated on the broadest reasonable interpretation given to the

phrase appearing in independent claims 16 and 20, wherein the phrase recites, "a memory

coupled to the processor, the memory *configured to store instructions for execution by the*

processor." Based on the reasonable broadest interpretation of the instant phrase, the data

processing systems of the claims need only comprise two (2) elements: a) a processor; and b) a

formatted memory which can store any program. Since the phrase does not require that the

memory **have** the instructions, but only be **configured to store** instructions set forth in the

claims, any formatted hard drive (or memory) would arguably be configured so that the

instructions (or program) set forth in the claims can be stored (MPEP 2106(II)(C), at 2100-8).

The dependent claims 17-19 further define the instructions which are not required to be on the

memory based on this interpretation.

Koza et al. disclose a computer system which comprises a processing unit and a memory

coupled to the processor (claim 27; column 23, lines 31-45).

Therefore, Koza et al. anticipate the invention as claimed.

As pointed out in *In re Mott*, 190 U.S.P.Q. 536 (CCPA 1975), "Claims must be given

broadest reasonable construction their language will permit in ex parte prosecution, and applicant

who uses broad language runs the risk that others may be able to support the same claim with a

different disclosure."

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all

obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 1-3, 5-10, 14, 16-18, and 20 are rejected under 35 U.S.C. 103(a) as being

unpatentable over Eisen et al. (Proc. Natl. Acad. Sci., USA, 1998, vol. 95, pages 14863-14868;

IDS reference) in view of Andrade et al. (Bioinformatics, 1998, vol. 14, no. 7, pages 600-607;

IDS reference) and Cocks et al. (U.S. Patent No. 6,607,879 B1, issued August 19, 2003, filed

February 9, 1998).

Claim 1 is drawn to a method of identifying a candidate gene from a plurality of

nucleotide sequences, the method comprising:

i)   obtaining gene expression profile data;

ii)   identifying (or selecting) a group of nucleotide sequences for further analysis;

iii)   using information extraction algorithms to retrieve and extract pathway

information of the selected nucleotide sequences;

iv)   cross-referencing the selected pathway information to related genes of other

species;

v)   viewing the cross-referenced information; and

wherein viewing said cross-referenced information facilitates the identification of a

candidate gene.

Preliminarily, Applicants are advised that the system claims, claims 16-18 and 20 are

drawn to a system comprising a processor and a formatted memory. Although Andrade et al.

disclose such a system (as evidenced by the executed computer algorithm which necessarily

requires a system comprising a processor and formatted memory), the present obviousness

rejection is made in order to facilitate the prosecution in that even if *arguendo* that the claimed

system is amended to require the recited programs, such system would nevertheless be,

considered obvious in view of the disclosure of the cited artisans.

Eisen et al. disclose a method of analyzing a group of genes (or nucleotide sequences)

selected from an expression pattern of a microarray (meets instant claim 10) comprising a

plurality of genes (or a plurality of nucleotide sequences) (Abstract). The method employed by

Eisen et al., with the aid of cluster analysis, groups genes of similar expression patterns together

(page 14865, 2nd column, 2nd paragraph) (meets instant claim 5). The method of clustering genes

is disclosed as being achieved in two ways: i) supervised; and ii) unsupervised (page 14863, 2nd

column, 2nd paragraph) and combination of the methods (page 14863, 2nd column, 2nd paragraph)

(meets instant claims 6-8). The functions of the grouped genes (or clustered) are further studied

to identify functions of the proteins encoded by the grouped proteins (meets instant claims 9).

Particularly, Eisen et al. disclose that an extensive cluster of 126 genes is strongly down-

regulated in response to stress which is dominated by genes encoding ribosomal proteins (112

genes) and other proteins involved in translation (page 14865, 2nd column, 3rd paragraph). Such

evidences that the further analysis has been done with the group of genes exhibiting similar expression pattern to identify the processes in which the genes were involved.

Although Eisen et al. evidences that further analysis is conducted for the grouped genes, such method is manually done and not through information extraction algorithms.

Eisen et al. do not extract pathway information of the selected genes

Eisen et al. do not cross-reference the pathway information and view the resulting information for facilitating the identification of a candidate gene.

Andrade et al. disclose an automated system and a method of searching texts of public databases for the identifying biological function of different protein sequences (Abstract). The method employs an algorithm which allows the searching of annotations of biological sequences in databases such as SwissProt, which contains protein pathway information (page 601, 1st column, 2nd paragraph) (meets instant claim 2). Andrade et al. disclose that the method queried for the word "ataxia telangiectasia" in MEDLINE database (meets instant claims 3,14, 17, and 18) which refers to a human disease associated with a disorder of particular *protein* and that the results obtained (or cross-referenced results) were directly related to the function of the protein and to its *genetic origin*, such as recessive, disorder, atm (the gene name), etc. (page 604, 1st column, bottom paragraph). All of the steps are accomplished through a computerized system executing programmed instructions, which would necessarily require a system comprising a processor and a computer memory (page 604, 2nd column, 4th paragraph) (meets instant claims 16-18, and 20).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to combine the teachings of Eisen et al. with that of Andrade et al. in order to

automate the process of searching the literature to identify the function of a candidate gene,
achieved through a computer system, with a reasonable expectation of success for the following
reasons.

One of ordinary skill in the art would have been motivated to automate the method of
Eisen et al., as expressed by Andrade et al., wherein the artisans state:

"Annotations of the biological functions of different protein sequences is a time-
consuming process currently performed by *human experts*. Genome analysis tools encounter
great difficulty in performing this task. Database curators, developers of genome analysis tools
and biologists in general ***could benefit from access to tools able to suggest functional***
annotations and faciliate access to functional information." (Abstract, motivation).

Andrade et al. continue to express the time constraints encountered when such task is
performed by human experts:

"Database annotations are commonly used by human experts as a first indication of
protein function. Perhaps the most frequent applications that rely on database annotations are
database similarity searches....The first information available is the protein name as described in
the sequence database entry, e.g. the DE line in SwissProt: 'rash_human, ras-p21 oncogene'. *A*
more detailed inspection requires manual access to other biological information annotated in
the database...Finally *deeper inspection of the available information would require the*
retrieval of the linked MEDLINE abstracts or direct consultation of the written bibliography.
The successful identification of the putative function of a protein often depends on the first steps
of search and, consequently, on the quality of the database annotations." (at page 601, 1st column,
3rd paragraph).

Andrade et al. disclose that their system which automates method for performing these

tasks would provide a first-aid tool for *retrieving information* and *suggesting functional*

annotations, useful for *investigation of functional relationship between proteins*, and could be

integrated into genome analysis system (page 601, 2nd column, 3rd paragraph).

Also, evidenced by Cocks et al., identification of the function of a gene by cross-

referencing literature sources is a well known technique in the art of functional genomic:

"To identify genes known to be associated with the regulation of blood cell biology, the

literature was surveyed and relevant sequences in GenBank and Lifeseq® database were

identified..." (column 19, lines 8-11).

Therefore, one of ordinary skill in the art, at the time the invention was made would have

been motivated automate the routine and manual method of searching the public databases

through the use of a system comprising an algorithm to further investigate the genes (per

Andrade et al.) that were selected from a gene expression assay performed by Eisen et al. with a

reasonable expectation of success. In *In re Venner,* 262 F.2d. 91, 95, 120 USPQ 193, 194

(CCPA 1958), courts clearly indicated that providing an automatic or mechanical means to

replace a manual activity which accomplished the same result is *not sufficient* to distinguish

over the prior art. (MPEP 2144.04(III)).

Therefore, the invention as claimed is obvious over the cited references.

Claims 1, 4, 11-13, 16-18, and 20 are rejected under 35 U.S.C. 103(a) as being

unpatentable over Eisen et al. (Proc. Natl. Acad. Sci., USA, 1998, vol. 95, pages 14863-14868;

IDS reference) in view of Ng et al. (Genome Informatics, 1999, vol. 10, 104-112; IDS reference)

and Cocks et al. (U.S. Patent No. 6,607,879 B1, issued August 19, 2003, filed February 9, 1998).

Claim 1 is drawn to a method of identifying a candidate gene from a plurality of

nucleotide sequences, the method comprising:

i)   obtaining gene expression profile data;

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iii)   using information extraction algorithms to retrieve and extract pathway

        information of the selected nucleotide sequences;

iv)   cross-referencing the selected pathway information to related genes of other

        species;

v)   viewing the cross-referenced information; and

wherein viewing said cross-referenced information facilitates the identification of a

candidate gene.

Preliminarily, Applicants are advised that the system claims, claims 16-18 and 20 are

drawn to a system comprising a processor and a formatted memory. Although Ng et al. disclose

such a system (as evidenced by the executed computer algorithm which necessarily requires a

system comprising a processor and formatted memory), the present obviousness rejection is

made in order to facilitate the prosecution in that even if *arguendo* that the claimed system is

amended to require the recited programs, such system would nevertheless be, considered obvious

in view of the disclosure of the cited artisans.

Eisen et al. disclose a method of analyzing a group of genes (or nucleotide sequences)

selected from an expression pattern of a microarray comprising a plurality of genes (or a

plurality of nucleotide sequences) (Abstract). The method employed by Eisen et al., with the aid

of cluster analysis, groups genes of similar expression patterns together (page 14865, 2nd column,

2nd paragraph). The functions of the grouped genes (or clustered) are further studied to identify

functions of the proteins encoded by the grouped proteins. Particularly, Eisen et al. disclose that

an extensive cluster of 126 genes is strongly down-regulated in response to stress which is

dominated by genes encoding ribosomal proteins (112 genes) and other proteins involved in

translation (page 14865, 2nd column, 3rd paragraph). Such evidences that the further analysis has

been done with the group of genes exhibiting similar expression pattern to identify the processes

in which the genes were involved.

Although Eisen et al. evidences that further analysis is conducted for the grouped genes,

such method is manually done and not through information extraction algorithms.

Eisen et al. do not extract pathway information of the selected genes

Eisen et al. do not cross-reference the pathway information and view the resulting

information for facilitating the identification of a candidate gene.

Ng et al. disclose a computerized system which performs the automated method of

discovering pathway systems from on-line text abstracts which as (GENBANK and MEDLINE),

which extracts relevant information from the free texts in the above databases, and presents the

extracted information *graphically* and intuitively (Abstract; Figure 3 (graph); claim limitation 4).

The method performed by the system of Ng et al. employs BioNLP, which processes the

scientific abstracts extracted by BioKleisli module, wherein BioNLP employs Natural Language

processing algorithms to identify protein names mentioned in the free texts; and performs

function word pattern matching (or comparison) to discover protein-protein relation expressed in

the abstracts (page 105; page 107; meets instant claims 11, 13, 16-18, and 20). The BiobNLP

algorithm is disclosed as employing template-filling technique (page 109, bottom paragraph),

allowing the user to specify the query of protein-to-protein relationship to be retrieved (as

defined in page 50 of the instant specification).

It would have been obvious to one of ordinary skill in the art at the time the invention

was made to automate the method of Eisen et al. with the teachings of Ng et al. in order to

automate the process of routine task of searching the literature to identify the function of a

candidate gene, achieved through a computer system, with a reasonable expectation of success

for the following reasons.

Ng et al. clearly provides the need (or motivation) to automate the process which is

routinely and arduously performed by scientists:

"The race to a new gene or drug is now increasingly dependent on how quickly a scientist

can keep track of the voluminous information on line to capture the relevant picture (such as

protein-protein interaction pathways) hidden within the latest research articles that are

continuously coming online from all over the world. To cope with this information explosion in

the electronic age, scientists *need a tool that would help them automatically scan the internet*

for research literature, extract the relevant knowledge from the (possible multilingual) free

text sources, and then present the information in an intuitive readable form" (page 104, 2nd

paragraph).

Ng et al. provides the description in which such need could be satisfied:

"We describe a prototype system for **automatic pathway discovery** from on-line text

abstracts, combining technologies that (1) retrieve research abstracts from online resources, (2)

extract relevant information from the free texts, and (3) present the extracted information graphically and intuitively" (page 104) which would be "a useful tool for routine and timely discovery of knowledge from online scientific literature, providing up-to-date accumulation of knowledge that is useful..." (page 111).

Also, evidenced by Cocks et al., identification of the function of a gene by cross-referencing literature sources is a well known technique in the art of functional genomic:

"To identify genes known to be associated with the regulation of blood cell biology, the literature was surveyed and relevant sequences in GenBank and Lifeseq® database were identified..." (column 19, lines 8-11).

Therefore, one of ordinary skill in the art, at the time the invention was made would have been motivated automate the routine and manual method of searching the public databases via use of an algorithm to further investigate the genes (per Ng et al.) that were selected from a gene expression assay performed by Eisen et al. with a reasonable expectation of success. In *In re Venner*, 262 F.2d. 91, 95, 120 USPQ 193, 194 (CCPA 1958), courts clearly indicated that providing an automatic or mechanical means to replace a manual activity which accomplished the same result is *__not sufficient__* to distinguish over the prior art. (MPEP 2144.04(III)).

Therefore, the invention as claimed is obvious over the cited references.

Conclusion

No claims are allowed.

Applicants are advised that the limitation of claim 15, which utilizes the scores of ranked publications for the ranking of pathway information extracted therefrom, is free of prior art and incorporating said limitation to the rejected base claims would make the claims free of prior art.
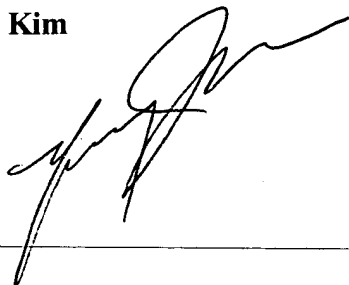
Inquiries

Any inquiry concerning this communication or earlier communications from the Examiner should be directed to Young J. Kim whose telephone number is (703) 308-9348 **(effective January 14, 2004, changed to 571-272-0785)**. The Examiner can normally be reached from 8:30 a.m. to 6:00 p.m. Monday through Thursday. If attempts to reach the Examiner by telephone are unsuccessful, the Primary Examiner in charge of the prosecution, Dr. Kenneth Horlick, can be reached at (703)-308-3905 **(effective January 14, 2004, changed to 571-272-0784)**. If the attempts to reach the above Examiners are unsuccessful, the Examiner's supervisor, Gary Benzion, can be reached at (703) 308-1119. Papers related to this application may be submitted to Art Unit 1637 by facsimile transmission. The faxing of such papers must conform with the notice published in the Official Gazette, 1156 OG 61 (November 16, 1993) and 1157 OG 94 (December 28, 1993) (see 37 CFR 1.6(d)). NOTE: If applicant does submit a paper by FAX, the original copy should be retained by applicant or applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED, so as to avoid the processing of duplicate papers in the Office. All official documents must be sent to the Official Tech Center Fax number: (703) 872-9306. For Unofficial documents, faxes can be sent directly to the Examiner at (703) 746-3172 **(effective January 14, 2004, changed to 571-273-0785)**. Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Young J. Kim

12/29/03